

CLAIM AMENDMENTS

1-31. (canceled)

32. (currently amended): A method of detecting post-transcriptional gene silencing (PTGS) of a target gene in an organism which method comprises the steps of:

detecting in a nucleic acid extract prepared from said organism in which organism it is suspected that PTGS is occurring to determine the presence as opposed to the absence of short RNA molecules (SRMs) which are 20-30 nucleotides in length in said extract,

characterizing any SRMs which are present in said extract wherein said characterizing comprises determining identity or similarity with said target gene,

wherein the presence of any SRMs having identity or similarity with said target gene indicates silencing of said target gene in the organism,

wherein said organism is selected from the group consisting of plants, insects, mammals, fish, reptiles and birds.

33. (withdrawn): The method of claim 32, wherein the organism is a plant.

34. (withdrawn; currently amended): The method of claim 32, wherein the organism is ~~a nematode~~ an insect or a mammal or a bird.

35. (previously presented): The method of claim 32, wherein the organism is a mammal.

36. (previously presented): The method of claim 32 wherein the SRMs are short antisense RNA molecules (SARMs).

37. (previously presented): The method of claim 32 wherein the SRMs are short sense RNA molecules (SSRMs).

38. (canceled)

39. (withdrawn): The method of claim 32, wherein the silencing of said target gene in the organism is associated with pathogen derived resistance.

40. (withdrawn): The method of claim 32, wherein the silencing of said target gene in the organism is associated with modification of a specific trait by co-suppression of the target gene.

41. (previously presented): The method of claim 32, wherein the step of characterizing any SRMs present in the extract to determine identity or similarity with a target gene is performed by a process that comprises:

tagging said SRMs with a marker, and
probing a library of genes from said organism, and
identifying the genes in said library that bind to said SRMs whereby a gene that binds to said SRM is identified as said target gene which is silenced.

42-48. (canceled)

49. (previously presented): The method of claim 32, wherein said short RNA molecules are 20-25 nucleotides in length.

50-65. (canceled)

66. (previously presented): The method of claim 32 wherein said determining identity or similarity comprises determining sequence identity or similarity.

67. (new): The method of claim 32 wherein the SRMs comprise both short antisense RNA molecules (SARMs) and short sense RNA molecules (SSRMs).